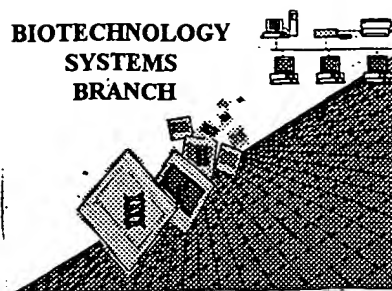


0590
0102



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/921,944A
Source: OIP
Date Processed by STIC: 1/2/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

OIPE

RAW SEQUENCE LISTING

DATE: 01/02/2002

PATENT APPLICATION: US/09/921,944A

TIME: 09:19:47

pp 1-2

Input Set : A:\ES.txt

Output Set: N:\CRF3\01022002\I921944A.raw

**Does Not Comply
Corrected Diskette Needed**

5 <110> APPLICANT: Battelle Memorial Institute

9 <120> TITLE OF INVENTION: Isolated Yeast Promoter Sequence and a Method of Regulated
Heterologous

10 Expression

14 <130> FILE REFERENCE: E-1823 CIP

16 <140> CURRENT APPLICATION NUMBER: 09/921,944A

18 <141> CURRENT FILING DATE: 2001-08-02

22 <160> NUMBER OF SEQ ID NOS: 10

26 <170> SOFTWARE: PatentIn version 3.1

30 <210> SEQ ID NO: 1

32 <211> LENGTH: 35

34 <212> TYPE: DNA

36 <213> ORGANISM: oligonucleotide

40 <400> SEQUENCE: 1

42 gctctagaca tatgagtagt ttccgtagta attga

35

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50 <211> LENGTH: 35

52 <212> TYPE: DNA

54 <213> ORGANISM: oligonucleotide

58 <400> SEQUENCE: 2

60 gctctagaat tactatactt ttaatcagct tcaga

35

66 <210> SEQ ID NO: 3

68 <211> LENGTH: 36

70 <212> TYPE: DNA

72 <213> ORGANISM: oligonucleotide

76 <400> SEQUENCE: 3

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84 <210> SEQ ID NO: 4

86 <211> LENGTH: 36

88 <212> TYPE: DNA

90 <213> ORGANISM: oligonucleotide

94 <400> SEQUENCE: 4

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36

102 <210> SEQ ID NO: 5

104 <211> LENGTH: 33

106 <212> TYPE: DNA

108 <213> ORGANISM: Oligonucleotide

112 <400> SEQUENCE: 5

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120 <210> SEQ ID NO: 6

122 <211> LENGTH: 33

124 <212> TYPE: DNA

126 <213> ORGANISM: Oligonucleotide

130 <400> SEQUENCE: 6

132 tctagaacta gttctatcaa actactccaa ata

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138 <210> SEQ ID NO: 7

140 <211> LENGTH: 33

142 <212> TYPE: DNA

RAW SEQUENCE LISTING

DATE: 01/02/2002

PATENT APPLICATION: US/09/921,944A

TIME: 09:19:47

Input Set : A:\ES.txt

Output Set: N:\CRF3\01022002\I921944A.raw

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160 <212> TYPE: DNA
162 <213> ORGANISM: Schwanniomyces castellii
166 <400> SEQUENCE: 8
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172 tttcagtggc cttaaaccag tccatcgaga cgacttcagc ctcttcgaga ccacaagggt 120
176 cgtttaataa ggaaatgaat agaatcacct ggagatattc gcagccatta atactatcaa 180
180 gtgaaaatcc tgaagaaaaa ttaattgcaa gatttttgac taatagtaaa ggtagtgaac 240
184 atgaaagtgg tattcaagtt aaatttttga ttaatgatcc tccactgaaa ttttctaagg 300
188 ctttatatct tgatgatgaa tcaacagagg ttcccttggt aaggaaatctt attagtggaa 360
192 gctacagcag tcattcttaa acatgattaa tgtctagatt tattggttat ttaggcattc 420
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200 tttaaagtag tgtttatagt ttttagtattg ttaacctttt tttcctaaat gttagtatgc 540
204 atgcttaaaa tgatgtcaga ggtagagtat gaattaattc cttttataaa tgctgttttg 600
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212 tttgagttcc aacgacaatc gaatgtattc atatagtagt tactacctta aacacaatcc 720
216 agatgggttta accaactgat gcctaagttt catgtggtgc tctttaacat cttttttgtc 780
220 ttcaaatctt aatgccatta gttcacatgt atatacgcca agagagtttt gtgaccaact 840
224 tacatttact agcaagtatt atctacaaag caaaaattac gacatatctg tgttggatcc 900
228 atcaactgtg gacacgaata acaagttccc aggattccta attattcaac tgccagataa 960
232 ataacatata tccaaagggt caacattatt taccaaattc aaagttggat tttgttaaat 1020
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244 ctaccttcta tcaactact ccaaatacaa gcggtctaaa atctacatgt aaatacctta 1200
248 ctgttacaaat tattctccct tgaattgacc aacctgacca tgaaaccttt ttggaatcag 1260
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288 aatccaatgg agcaacaatg agagatctac attttaaacc ccagtctact ccagatattg 1860
292 gagtataacc ccattcttac cgttatatcc atgacccgca tcgaaatttt caaaggattt 1920
296 cgaggaaatt ctttctctaa atacgaagtg ttattggtga ttcaattact acggaaacta 1980
300 ctccattatg gatgtagagt tggatgaatg agcgcaattg taatttgcca agttatagta 2040
304 atagtttggc aaactggaga atttttcatt attgggaaaa tataaataaa ggcaagtatc 2100
308 cattgaaatt ttaaaaatga actcatgact gtattataac aagcaagatg atttttctga 2160
312 agctgattaa aagtatagta at
318 <210> SEQ ID NO: 9
320 <211> LENGTH: 328
322 <212> TYPE: DNA
324 <213> ORGANISM: Schwanniomyces castellii

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RAW SEQUENCE LISTING

DATE: 01/02/2002

PATENT APPLICATION: US/09/921,944A

TIME: 09:19:47

Input Set : A:\ES.txt

Output Set: N:\CRF3\01022002\I921944A.raw

328 <400> SEQUENCE: 9:

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330 agatctacat tttaaacccc agtctactcc agatattgga gtataacccc attcttaccg      60
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338 acgaagtgtt attggtgatt caattactac ggaaactact ccattatgga tgtagagttg      180
342 gtgaatgtag cgcaattgta atttgcgaag ttatagtaat agtttggcaa actggagaat      240
346 ttttcattat tgggaaaata taaataaagg caagtatcca ttgaaatttt aaaaatgaac      300
350 tcatgactgt attataacaa gcaagatg                                     328

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356 <210> SEQ ID NO: 10

358 <211> LENGTH: 325

360 <212> TYPE: DNA

362 <213> ORGANISM: Schwanniomyces castellii

366 <400> SEQUENCE: 10

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372 ttatatccat gaccgcgcatc gaaattttca aaggatttcg aggaaattct ttcctaaaat    120
376 acgaagtgtt attggtgatt caattactac ggaaactact catatggtag tagagttggt      180
380 gaatgtagcg caattgtaat ttgcgaagtt atagtaatag tttggcaaac tggagaattt      240
384 ttcattattg ggaaaatata aataaaggca agtatccatt gaaattttta aatgaactca      300
388 tgactgtatt ataacaagca agatg                                     325

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/921,944A

DATE: 01/02/2002

TIME: 09:19:48

Input Set : A:\ES.txt

Output Set: N:\CRF3\01022002\I921944A.raw

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/921,942A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/921,944A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.